

Query 276 YLEENVMHFLDAATAVAAROTTVISHSPNTSYDTALLEARIOEEELMANKRLDM 335
 233 RRMNNAAPSSDSSLSAPLPEYSSCOPPSAPPSPPIAKYISAPVSDATPDY----- 283
 QY 336 EGRIKTLHAQIIEKDMIKVLAQSRKREPKTEOLSCMRPA--KSLMSINAGSGLSHS 393
 283 -----AVTAL-----PPTSTPTPLRHAATREATSLGSAFHPVLPHY 321
 QY 394 SLTNGSPIMEEKRDKSMKSGSLGILLGDIYRAEYVPSPT----- 433
 322 AYV-RPLNKNR-----PSSPVNTPTSSOPPAKSCAMPSTNF 358
 QY 433 SPVPSTPLLSAH---SKTGRDCSTOTERTGESNKTAAVAPISVPAAVAAAATA 489
 359 SPLPSPPIIMSSPPGKATGR-----PVLPCVSSFPQMPSP--TA 400
 QY 490 TAAITTTTVAAPVAVAAAAAP-----TAAAAASP 520
 401 PNGSLDSVTYVSPPTSGPAAPPPEPPPPPLPPLPLPLASLHSCSOASPP 460
 QY 521 ATAATAAASPAAGQIPAAASVSAANAAP-----SAAAAAAYVAPADAPVPAP 573
 461 GTPLASIPSSKPSV---LPSPSAGAPASAEPLNPELGSSASEPGLQAA-SQPAESPTP 516
 QY 574 -ALV---PVPAAPAAQASAPAOQAPTSAPAVAPTPPTPPPAVAAQAEVPASPTGCPH 629
 517 QGLVLGGPAPPPPPPLPSGPAY-----ASALPPPGPPPPPL-----PSTGPPPP 562
 QY 630 RLSPSLTCNPDKTGP-----VFHSNTLEKRTPI 659
 563 PPPPPL---PNOAPPPPPPPAPPLPASGIFSGSTSDNPL 602

RESULT 2
 W37153
 ID W37153 standard; Protein; 802 AA.
 AC W37153;
 DT 06-JUL-1998 (first entry)
 DE Mouse neural Mena+++ protein.
 KW Neural Mena+++ protein; mammalian Ena; Enabled protein; Evi protein;
 KW cytoskeleton; cell morphology; cell adhesion; cell differentiation;
 KW cell growth; cell motility; mouse.
 OS Mus musculus.
 PN M09801755-A1.
 PD 15-JAN-1998.
 PF 03-JUL-1997; 011669.
 PR 05-JUL-1996; US-675815.
 PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 PI (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 PI Gertler FB, Niebuhr K, Soriano P, Wehland J;
 DR WPI: 98-101197/09.
 PT Detection of modulators of Mena and Ena-VASP-like genes and proteins
 PT used in control of cytoskeletal dynamic events in normal and
 PT abnormal cell morphology, adhesion, motility, growth and
 PT differentiation
 PS Example 4: Page 63-65; 77pp; English.
 CC This protein comprises novel murine neural Mena+++ . Its amino acid
 CC sequence was deduced from a cDNA clone obtained from a mouse brain
 CC cDNA library. Two other isoforms, neural Mena+ (see W37151) and
 CC neural Mena++ (see W37152), are also disclosed. Unlike mammalian
 CC Ena (Mena, see W37148), neural Mena isoforms exhibit neural
 CC tissue-specific distribution. Based on the disclosed Mena and Evi
 CC genes (see also V02996-98) and proteins (see also W37148-49), a
 CC variety of methods and compositions are provided for screening,
 CC isolating and characterising endogenous and exogenous factors,
 CC drugs and therapeutic agents useful to evaluate and/or control
 CC cytoskeletal dynamic events involved in normal and abnormal cell
 CC morphology, adhesion, motility, growth and/or differentiation. A
 CC method of detecting a modulator of Mena activity/expression is
 CC claimed.
 SQ Sequence 802 AA;

Query Match 6.88; Score 229; DB 1; Length 802;
 Best Local Similarity 20.48; Pired. No. 1,7e-06;
 Matches 134; Conservative 89; Mismatches 205; Indels 228; Gaps 28;

QY 98 FNRDLRRLTANKO-LAEYEGSEDT-----KTSOLF--KKKESQREK 142
 DB 100 FASAMMALELYLSOEAQSKVATQDSTLRCIFGCPPLPRONSQPLPAOVNGPQSEEL 159
 QY 143 EKLAEELATARSTNEDORRHIEIRDAQLSNAQKVVLEELKKQYVVKVMOQALV 202
 DB 160 EIQRRQL-----QEQRRQKLEERERERERLERERLERERLERER 204
 QY 203 QLOAACKRQLEHRLTLERLESLRQOQRCOPTVSEYNAALMELLREKERI 262
 DB 204 QLEORQERHVERLERERLERERLERERLERERLERERLERERLERER 238
 QY 263 LALEADMTKEQYVLEENVMHFLDAATAVAAROTTVISHSPNTSYDTALLEARIOKEE 322
 DB 239 EQLREQEVERERERKSNAAAPSSDSSLSAPLPEYSSCOPPSAPPSPPIAKYISAPVSDAT 298
 QY 323 EELMANKRLDMEGRIKTLHAQIIEKDMIKVLAQSRKREPKTEOLSCMRPA--KSLM 380
 DB 299 PDV-----AVTAL-----PPTSTPTPLRHAATREATSLGSAFHPVLPHY 327
 QY 381 SISNAGSGLSHSSTLTGSPIMEEKRDKSMKSGSLGILLGDIYRAEYVPSPT----- 433
 DB 328 SLGSAFHPVLPHYATVP-RPLNKNR-----PSSPVNTPTSSOP 364
 QY 433 -----SPVPSTPLLSAH---SKTGRDCSTOTERTGESNKTAAVAPISVPA 476
 DB 365 PAAKSCAMPSTNFSPPLPSPPIIMSSPPGKATGR-----PVLPCVSS 408
 QY 477 PVAAATTAATITATTTTVAAPVAVAAAAAP----- 513
 DB 409 PVPQMPSP--TAPNGSLDSVTYVSPPTSGPAAPPPEPPPPPLPPLPLPLA 466
 QY 513 -----AAAAAPSPATAATAAASVPAAGQIPAAASVSAANAAP-----SAAAAAAY 560
 DB 467 SLHSCSOASPPPGTPLASIPSSKPSV---LPSPSAGAPASAEPLNPELGSSASEPGL 523
 QY 561 QVPAAPAPVPAP-ALV---PVPAAPAAQASAPAOQAPTSAPAVAPTPPTPPPAVAAQAEVP 616
 DB 524 QAA-SQPAESPTPGQVLGPAPPPPPPLPSGPAY-----ASALPPPGPPPPPL--- 574
 QY 617 EVPASPTGPGPHRLSPSLTCNPDKTGP-----VFHSNTLEKRTPI 659
 DB 574 -----PSTGPPPPPPPL---PNOAPPPPPPPAPPLPASGIFSGSTSDNPL 621

RESULT 3
 W37152
 ID W37152 standard; Protein; 787 AA.
 AC W37152;
 DT 06-JUL-1998 (first entry)
 DE Mouse neural Mena+++ protein.
 KW Neural Mena+++ protein; mammalian Ena; Enabled protein; Evi protein;
 KW cytoskeleton; cell morphology; cell adhesion; cell differentiation;
 KW cell growth; cell motility; mouse.
 OS Mus musculus.
 PN M09801755-A1.
 PD 15-JAN-1998.
 PF 03-JUL-1997; 011669.
 PR 05-JUL-1996; US-675815.
 PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 PI (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 PI Gertler FB, Niebuhr K, Soriano P, Wehland J;
 DR WPI: 98-101197/09.
 PT Detection of modulators of Mena and Ena-VASP-like genes and proteins
 PT used in control of cytoskeletal dynamic events in normal and
 PT abnormal cell morphology, adhesion, motility, growth and
 PT differentiation
 PS Example 4: Page 60-63; 77pp; English.
 CC This protein comprises novel murine neural Mena+++ . Its amino acid

Query Match	6.8%	Score 228.5	DB 1	Length 787
Percent Local Similarity	21.28%	Pred No. 1.8e-06		
hes 136; Conservative	84;	Mismatches 206;	Indels 217;	Gaps 28;

RESULT 4
R72826
ID R72826 standard; Protein: 2482 AA.
AC R72826;
DT 27-FEB-1996 (first entry)
DE Human mitotin.
KW Cell cycle; M phase; mitotin; retinoblastoma; mitosis; cell growth;
inhibition.

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Query Match      6.8%   Score 226.5   DB 1,   Length 2482;
Best Local Similarity: 21.4%   Pred. No. 1e-05;
Matches 139;   Conservative 100;   Mismatches 233;   Indels 179;   Gaps 26

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01 26 QOMTEISDENRULROELE-----GCYKARALQVETELORVSEAVENLVKSSKRE 78
02 1948 QDTLEVLOSSYKMINLELELTETKDKMSFEYKVNKMTAKETELOR--EHEMOMQKAELOE 20050
03 79 ALFKAMNKLEGELEJRRHHD-----PNRDLRERLEFANKOLAEKVEYGSDD 124
04 2306 FL-SGENNRLAGELQULLELEIKSSKOQLELLENSELKSLDCKHKKOQVEKGVAREI 20644
05 124 -----TRFTISQLEFANKNESOREKEKLEAEIATARSTNEDJRRHIEI---RDQAL 170
06 2065 AEYOLRLEHAEKHOALLDITNKQYEVETQYTRKULTSREKETSQKLEIDILKSKREL 21244
07 173 SNAQAKVVKLEELKKRYV---YVDKV---EKMOQALVOLQANACERBOLEHRLRL 222
08 2125 NNSLKATQOTLEELKTKTKDNKLKNNYVOLAKRENERAOGKKRLIKSCOLEEKEKITLOEL 21844
09 223 ERELESLRIOROGNOCQPTVSEYNA--AALNELRKEKEEILALEADMTKQEOXYLEEN 280
10 2185 S-QQANQOEKQGTGYMDIKYDBELTEIKEKLETLEEK-----TREADEYIDKY 22322
11 281 VMRHEALDAATVAAQORPTVISHSGPNTSYDTALEARIQKEEETILMANCKRLDMEGRK 340
12 2233 C-----SLLISHE-----KLEKAKEM-----LETOVA 22544
13 341 TLHROILEKKA-----MIKVLOQRSKREPKTEOLSMOPRAXKMSISNAGSGLSHSTL 396
14 2255 HLCGQSKQKQSRSPILGVPVPEPSPISVTE-----KLSGQNKAKSKRORSSGI 23064
15 397 TGSPTMEERKDDKSMKSGSLGILGGYVRAEYVPTSPVPSPPTPLLSHAKSTGSHDCSTQ 456
16 2307 -----FENG-----GG-----PTPTPSPSPFKSKKKVMSTIHAIF 23374

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FT /label= Extended_coiled_structure
 FT 1850..2990
 FT /label= Extended_coiled_structure
 FT 3048..3248
 FT /label= C-terminal domain
 FT /note= "the C-terminal domain is predicted to
 FT form a proline-rich (10.6%) highly
 FT basic (pI 10) globular domain"
 PN MO9617867-A1
 PD 13-JUN-1996
 PF 08-DEC-1995; U16216.
 PR 09-DEC-1994; US-353700.
 PA (FOXC-) FOX CHASE CANCER CENT.
 PA (UYVE-) UNIV TECHNOLOGIES INT INC.
 PI Ratner JB, Yen TJ.
 DR WPI: 96-287116/29.
 DR N-PSDB: T34578.
 PT - DNA encoding kinetochore protein - used as a marker for the G2 and M
 PT phases of a cell cycle, partic. for detection of malignant diseases
 PS claim 12: Page 41-54; 7pp; English.
 CC A 372 kDa human kinetochore protein, CENP-F (R39795), is detected
 CC by immunofluorescence microscopy only during the G2 and M phases
 CC of a cell cycle. It is the product of a cDNA clone (734578)
 CC isolated from a breast carcinoma CDNA library. Recombinant CENP-F
 CC can be produced by expression in prokaryotic or eukaryotic host
 CC cells. CENP-F can be used to detect autoimmune antibodies to
 CC the protein, which may provide an early diagnosis for the onset
 CC of various malignant diseases. Use of CENP-F as a cell cycle
 CC marker allows the specific detection of G2 and M phase cells.
 SQ Sequence 3248 AA;

Query Match 6.7%; Score 225; DB 1; Length 3248;
 Best Local Similarity 21.4%; Pred. No. 1.8e-05;
 Matches 110; Conservative 106; Mismatches 167; Indels 132; Gaps 21;

QY 20 AIVSAOQWELISDENRNLROLEGCEYKVARLOK-----VTEIQRVSEAYE 68
 DB 2103 AEVKEKTELQTLSSDVSELKDKTHLOEKLSLEKDSQALSLTNCLENOIAQNKKE 2162
 QY 69 NLVKKSSK-----REALKAMKNGLEGEIR-----RMHDFNR---DLRE 104
 DB 2163 LLVKESESLQARLSSEDEKLVNSKALEALVEKEGFALRLSSTOEVHQLRGIEKLRY 2222
 QY 105 RLETKANKO---LAER-----EYEGSEDTKRTISOLFAKNKESQR---EKELEAEIAT 151
 DI 223 RLEADEKQOLTAETKLERERENDSLKQVENLERELQWSENOELVILDAENSKAEVET 2282
 QY 152 ARSTNEDQRRHIEIDQALNSNAQAVVVKLEELKKQYVAVKEM-----QQA 200
 DB 2283 LKTOLEEMARSLKTELVDLVTLRSEKENTQIOERQOGLSELKLSFSKLEEKSDA 2342
 QY 201 LVQLQ-----AACERK-----OLEHRLRTLRBRE 225
 DB 2343 ELQIKESKTAVENTLONLKEINAVALCGQELMKATEOSLDPIEEHOLRSTIKEL 2402
 QY 226 LESLRIOQRGNC--QPTNVSEFYNAAL-----MELLREKEERILAEADMTWE 273
 DB 2403 RARLEADEKQOLCYQOKESEHNDLKRVENLERELIARTQNH-AALEANSNGE 2461
 QY 274 QKYLEENV-----MRHVALDAAA-----TVAAGDDTVYISNP--NYSYDTALEAR 317
 DB 2462 VETLAKTEGNTOSLRLGELDVLTIRSEKENLTNELQKEOERISLELEIINSFENILQ-- 2520
 QY 318 IOKEEELIMANKRLDDEGRITLHAQIIIEKAMITVLOORSR-KEPSKTEQOSC-MR 374
 DB 2520 -EKDEKQVOMEKSTANE-MQIOLKELNRYVALHNDQEKACKQONLSOVECELE 2577
 QY 375 PAKSLMSTISNAGSLSSSTLTGSPIMEERDDK 409
 DB 2578 KAOLLOGIDEAKNNYIVLQSSVKG--LQOEVEDGK 2610

RESULT 7
 W6540
 ID W26540 standard; Protein; 442 AA.
 AC W26540;
 DT 12-JAN-1998 (first entry)
 DE Trypanosoma cruzi antigen TcH129.
 KW Antigen; epitope; vaccine; protective immunity; Chagas disease;
 KW diagnosis; therapy; immunosay.
 OS Trypanosoma cruzi; Tulanean strain C2.
 PN WO9718475-A1
 PD 22-MAY-1997
 PF 14-NOV-1996; U18624.
 PR 14-NOV-1995; US-557309.
 PA (CORI-) CORIXA CORP.
 PA Houghton RL, Lodes MJ, Reed SG, Skeiky YAM;
 PI WPI: 97-289413/26.
 DR N-PSDB: T69165.
 PT Diagnosing Trypanosoma cruzi infection by detecting antibodies to
 PT novel antigens - which are useful in vaccines to provide protective
 PT immunity against Chagas' disease
 PS Disclosure; Page 80-82; 110pp; English.
 CC This polypeptide sequence comprises full-length antigen TcH129 of
 CC Trypanosoma cruzi, identified by sequencing a DNA clone (see T69165)
 CC obtained by screening a Trypanosoma cruzi genomic expression library
 CC with pools of sera from infected individuals. T. cruzi antigens
 CC (see W26530-41), or epitope-containing repeat sequences (see W19094-
 CC 102; W19079-86 and W26542-44) of native antigens, can be used in a
 CC variety of immunoassays for detecting T. cruzi infection in a
 CC blood serum, plasma, saliva, cerebrospinal fluid or urine sample.
 CC The polypeptides are also useful in vaccines and pharmaceutical
 CC compositions for inducing protective immunity against Chagas
 CC disease. They can be produced by expression in transformed or
 CC transfected host cells. TcH129 is a polymorph of the T. cruzi
 CC TCE epitope repeat sequence (see W19063).
 SQ Sequence 442 AA;

Query Match 6.5%; Score 216; DB 1; Length 442;
 Best Local Similarity 44.9%; Pred. No. 5e-06;
 Matches 71; Conservative 7; Mismatches 58; Indels 12; Gaps 6;

QY 476 APVAATAATTAATTTTMYAAVAVAAAAAPAAAPATAATTAATAVSPAA 535
 DB 281 AAAAKQKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 338
 QY 536 GQIPAAASVAAAANAVPSAAAAAANAVAPAPAV---PAPALVPVPPAAA---QASA 588
 TL 339 AAPPAKAAAPPAKTAAPPAKTAAPPAKAAAPPAKTAAPPAKTAAPPAKTAAP 397
 QY 589 PAQTOAPTAPAVAPPAVPPAPPTPAVPAQAEVAPASATGP 626
 DB 398 PAKAAAPPAKAAAPPAKAAAP-PAKAAAP-PAKAAAP 433
 EMBL 8
 W60024
 ID W00024 standard; Protein; 1972 AA.
 AC W00024;
 DT 25-MAR-1997 (first entry)
 DE Smooth muscle myosin heavy chain SMI isoform protein.
 KW Smooth muscle; myosin heavy chain; SMI isoform; rabbit; arteriosclerosis;
 KW gene therapy; mouse; SM2 isoform; retrovirus; adenovirus; restenosis;
 KW associated adenovirus; coronary artery catheterisation; sclerotic artery.
 OS Mus musculus.
 PN W06962:065-A1.
 PD 01-AUG-1996.
 PR 23-JUN-1996; J00134.
 PA (OSAP) OSAKA PREFECTURAL GOVERNMENT.
 PA (YESS-) VESSEL RES LAB CO LTD.
 PI Takawa E, Hasegawa K, Ishiyama H, Matsuda Y, Oda S;
 PI Sugawara M, Takahashi K;
 DR WPI: 96-362693/36.

CC pathways that involve the proteins, particularly cancer (e.g. leukaemia
 CC and lymphoma), while modulators of ALK-7 (which is a type I receptor
 CC serine/threonine kinase) are used to promote neuronal survival,
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the
 CC proteins can be used as probes to identify and clone related sequences;
 CC to detect protein-encoded RNA; to generate transgenic animals and in
 CC gene therapy (optionally after mutation). Ab are used to determine the
 CC proteins.
 SO Sequence 1274 AA;

Query Match 6.3%; Score 212.5; DB 1; Length 1274;
 Best Local Similarity 20.7%; Pred. No. 3.1e-05;
 Matches 151; Conservative 104; Mismatches 306; Indels 167; Gaps 30;

QY 25 AQQVEIISDENRLROELGCEYE-KVARLQKVEIQRVSEAYENL-VKSSSKREALEK 82
 D 3 AHEASSIYSEKAKLIREMAKTEKEDKNEVLQFMDSMDDEPTVNDLAYSHPQLMEK 62
 QY 83 -----AARN-----KLEGEIRRHNDNRDLERLETANNQLAKKEYEGSEDTKRT 127
 DB 63 CAALSVRDYTRNIVQSMQVLGVFTDVEASLKDIDLE--EDELLEKQFO-----EA 114
 QY 128 ISOLFANKRESOREKLEELA-----TARSTNEQORHIEIR-----DQA 169
 DB 115 VQAGALSIYSKALAEVRRMAKMEYHEKASFNSLHRAHMLHVGNLLSGPLDQV 174
 QY 170 LSNQAQAVKLEELKKQYVVDYKEMQALVOLQACERQDELHRTLRLELESL 229
 DB 175 RAALPTALSPEDKA-----VLQNLKRLAVQEHDRQVLSLQQLRLQKD----- 223
 QY 230 RIQROGNCPTNINSEVNAALMELKEKERITALEADMTKMDQ--KYLEENVMRHEAL 287
 DB 223 -----DITASLVTTDISEMKKL-FEELQKKYDQLKYLQNLAAQDRV 264
 QY 288 DAAT-----VAQRDTVISHSPNTSYDR-----ALEARIQKEBEELIMANKRLCLDM 335
 DB 265 LCALTEANVOYAAVRVLSLDOKKWNSTLOTLVASYEYEDLMKKSQE---GRDFYADL 320
 QY 336 EGRIKTL-----HAQIIEKDMIKVLOORSREKPEKTLQSLSCMRPAKSLMS 381
 DB 321 ESKVAALLERTQSTCOAREARQOLLRE-----LKKPRPRPTAHPRLPRRESEAVE 375
 QY 382 ISNAGSGLSHSSTLTGSPIMEERKDKSMKSGSLGILLGGDYARAEVYPTSPSPYPTPL 441
 DB 376 AGRPPELRLSLPDMVAGPRLPD-----TFLGS-----ATPLHPPSPSPST-- 419
 QY 442 LSAHSKSGSDCSOTRGESNKTAAVAPISVAPYA--AAATAAIIYTAATITTTMV 499
 DB 419 -----GGPHYLSGLRPPGYTSGTQDIQ-RAGPHAMPVAPGALYPPAYPELGLV 472
 QY 500 AAAPVAVAAAAPAAAAAPATATAAATAAASPAAGOI-----PASAASAASAAVAPSA 554
 DB 473 PRSSPQHGVSVPYVGGRAPVAGLSPAPRPGSGPELMAAVRAPATYTDVSIQAPISPH 532
 QY 555 AA-----AAAVOVAPARAPVAPALVVPAPAAQASAPAO-----TQAPTS--APAVAPT 604
 DB 533 TAPRPNTAPRPPECFEVRPPQPLRPYTYRAGAKQPIPAQNHSSSIPGIFAPRIPQ 592
 QY 605 PAPTTPAVAOAEVAPSPATGPRGHRISISLNCNPKTGRVPHSTLERKPTIO----- 661
 DB 593 PQRHPQRHPSQAGPQRPQO--PLRLQHPHLF--PQOAG-----LLRPGSPYRYPAQ 641
 QY 661 --ILGOEP 666
 DB 642 PGVLGQPP 649

RESULT 11
 W02258
 ID W02258 standard; Protein: 1411 AA.
 AC W02258;

DT 09-MAR-1997 (first entry)
 DE Nucleolar/endosomal auto-antigen p162.
 KW Auto-antibody; p162; rheumatic disease; antigen; diagnosis;
 CC gene therapy.
 CC Homo sapiens.
 CC DE19515514-C1.
 DB 12-SEP-1996.
 PF 27-APR-1995; 015514.
 PS 27-APR-1995; DE-015514.
 PA (PRIV-) PRIVATES INST IMMUNOLOGIE & MOLEKULARGEN.
 PI Renz M, Seelitz HP.
 DR WPI: 96-403153/41.
 DR N-PSDB: T58751.
 PT DNA encoding nucleolar-endosomal auto-antigen - useful for exact
 PT diagnosis of rheumatic disease, in gene therapy and for removal of
 PT specific auto-antibodies
 PS Claim 1, Fig 2; 15pp; German.
 CC Transformed cells can be cultured to produce the antigen p162, for use
 CC in exact (differential) diagnosis of rheumatic disease, i.e. they
 CC can detect, in immunoassays, Western blots, etc., rheumatism-
 CC specific auto-antibodies. The antigen can be used therapeutically,
 CC in the removal of auto-antibodies from the circulation, or when
 CC coupled to a cytotoxin, the elimination of auto-antibody-
 CC producing lymphocytes.
 SO Sequence 1411 AA;

Query Match 6.3%; Score 211; DB 1; Length 1411;
 Best Local Similarity 22.2%; Pred. No. 4.4e-05;
 Matches 108; Conservative 75; Mismatches 155; Indels 148; Gaps 17;

QY 30 ELSDEN--ENLROELGCEYKVARLQKVEIQRVSEAYENLVKSSSKREALEKARNK 87
 DB 328 FASVSKNIQATIRKDKDCCQQLQSLASSETSLRH--VLESEKGAQKLEEL 381
 QY 83 LEEGIRRHNDNRDLERLETANNQLAKKEYEGSEDTKRTISOLFANKRESOREKLEELA 147
 DB 382 SEVEETKQYH-----LKAFFQLOQQQREKQHGID--LQSEINQSHSLLETROLGARHG 435
 QY 148 ELTARSTNEQORHIEIRQALSNQAQAVKLEELKKR-----QYVVDYKEM-- 198
 DB 436 RLKEORQLSSEK---LMDKEQVADLQKLRLSEDLKEKYTNSTELQHOLDTKQOHOE 492
 QY 198 QOALVOLQAA--CEKREQLRHLR-----TRERELESL--R 230
 DB 493 QOALQOSTTKLREAOQNDLEQVRLQIGDKDKTONLEALLQKSKENISLLEKEREDELYAK 552
 QY 231 IQORQNC-----QPT-----NVSEYNAALMEL-----LREK 258
 DB 553 IQAGEGTAVLNLOEKKNHTLOEQVOLTPEKLNQSESHQAOENLHDQVQOQAKHLRAA 612
 QY 259 EERITALEADMT-----KWEQKYLEENVMRHFALDAATVAAQR----- 298
 DB 613 QDRVLSLETISVNLNSQLNESKEKVSQLDIQIKAKTELLLSABAATAQADLQNHDTA 672
 QY 298 -----DTTVISHSPNTSYDPTALRLARIQKEEELIMANKRLCLDMEGRT 339
 DB 673 QNALQDYQOELNKTITTOLODVWAKLQDKOEHCSQLESHKYEKYLSTQKTEELEGOI 732
 QY 340 KTLHAQITIE--KDAIKVLOORSR-----KEPSKTEQLSCMRPA 376
 DB 733 KRLFAISLEFKASKQALQDLOQQRQRLNDLDELRLATLSKOLEMEKEIYSTRLDQKKS 792
 QY 377 KSLMST 382
 DB 793 EALEST 798

RESULT 12
 W7734
 ID W76734 standard; Protein: 1315 AA.
 AC W76734;
 DT 15-JAN-1999 (first entry)

DE Human mdia Rho targeting protein.
 KM Rho protein; mdia; mammalian diaphanous; target protein; human;
 KN Rho protein-combining; proline-combining; chromosome 5q31.2; disease;
 KM respiratory tract; oversensitivity; bronchial asthma; marrow leukaemia;
 KM marrow dysplasia syndrome.
 OS Homo sapiens.
 PN J10262680-A.
 PD 06-OCT-1998.
 PF 25-MAR-1997; 090170.
 PR 25-MAR-1997; JP-090170.
 PA (KIRI) KIRIN BREWER KK.
 DR WPI: 99-002481/01.
 DR N-PSDB; V62933.
 PT Human Rho target protein and its gene - useful for elucidation of
 mechanisms of respiratory tract disease
 PS Claim 2a; Page 28-31; 54pp; Japanese.
 CC This sequence represents a human Rho target protein, mdia (mammalian
 diaphanous). This protein has active type Rho protein-combining ability,
 has proline-combining ability, has a M.W. of 150 kDa measured by sodium
 dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) and its
 gene is positioned at human chromosome 5q31.2. The nucleic acid can be
 used for the recombinant production of the protein. The protein is useful
 for the elucidation of mechanism of diseases such as respiratory tract
 CC oversensitivity, bronchial asthma, acute marrow leukaemia and marrow
 CC dysplasia syndrome.
 CC Sequence 1315 AA.

Query Match: 6.3%; Score 209.5; DB: 1; Length 1315;
 Best Local Similarity 20.5%; Pred. No. 5e-05;
 Matches 163; Conservative 97; Mismatches 280; Indels 257; Gaps 39;

QY 7 SSASYQVPV ADPFAVSRQQNV EILSDERN LROELGCEYK 49
 DB 114 SSASYQDDPTAOSKQVDSQVLFPEOMLDMNEKQOPLKENDIIKREWSQYLY 173
 QY 50 VARLOKVFETIORVSEAYENLVKSS SKREALKAMRN K 87
 DB 174 TTSAGHSQKSSSSAMMYIOELNSGLDMPLESLSLVSNPNVSWQVTEAGELAS 233
 QY 88 LEEGIRMDNFNDLRRLTETANKQALKEKEYEGSEDTRK TISQLEPAKKNSQREK 142
 DB 234 LLDILRLHDE EKEETA GSYDRNNHRIICAKAMNNKFG 274
 QY 143 EKEELATPASTNEDORRIETRDQALSNQAQVKL EEEELKK 188
 DB 274 IKTLEETEGLLVRAADPAVPMMDAALSLALCILPQEDMNERVLEAMT 327
 QY 188 QYVVDKVEKMOAL VOLOAC EKREOLEHRLRRL 224
 DB 328 ERAMDEVERFOPLDGLKSGTTIALKVGCLQINLITPAEELDFVHTRSELMRLGLH 387
 QY 224 RELES LRIO ORQGNCP TNSVYNAA ALMELLREK 258
 DB 388 QVLQDLREIENEDMRYQLNVFDEGGEDSDYDLKGRDDIMEMDDFNEVYQILLNTYKDS 447
 QY 259 E ERLALEADMTKEQK LEENV MRFPALDAAT 292
 DB 448 KAPHEFLSLQHLILVNRNDYEARPOYYKLEECISQVLHKNQADDPFKRHQIIEGL 507
 QY 293 VAAQRDTTVISHSP NTSYDTALEARIQKEEELIMANKRCIDMGRKIKTLHAQI 346
 DB 508 IDQIMDKTVERKEAKAELEKLDSELTARHELOVEMKKNES DEQKLODDQG 552
 QY 347 IENDAMIKVLOORSRKPEKTEQLSCMRPAKSLMSISNAGSLSHSSTLTG SPIMEE 404
 DB 562 EKDAL HSEKQOINTER QDLEAEISQLTGVAKLTNE 597
 QY 405 KRDDKSMKSGSLGLGVDYAEVYPTPS PYPSTPLLSAHSKTSGRDCSTQTERGE 462
 DB 598 LEQAKKEMSLAA AITVPVSPVSPAPVPPAPPL PGDSGT 638
 QY 463 SNKTAAVAPISVPAPVAAATAATATATITTTWAAAPVAAAAAPA AAAA 517

DB 638 ILPPPPAPGST IPPPPPPPPPPLPGGVCISSPSSLGCRATISP 684
 QY 518 PSAPRAAATAAASPAAG QIPAAASVASAAVAASAAAAAQAAPAPAPVAPA L 575
 DB 685 PPLSGDARTIPPPPLPEGVGRPSSSLPGCTALIPPPPLPGSART PPRPPPLPGSAGI 743
 QY 576 VPAPAPAAQASPAQOTQAPTSAPAVAPTP AAPPTPAVAQAE VPAS 621
 DB 744 PPPPPPLPGGAGMPPPPPLPGGPGIPPPPPPGCGIPPPPGMGMPPPPFGVPA 803
 QY 622 PAT GPGPHRLSTPSL 636
 DB 804 PVLPGILTPKLTKEPV 820

RESUI: 13
 W63043
 ID W63043 standard; Protein: 561 AA.
 AC W63043;
 DT 26-OCT-1998 (first entry)
 DE Streptococcus uberis bovine lactoferrin binding protein.
 KM Bovine lactoferrin binding protein; LBP; mastitis; vaccine;
 KM diagnosis.
 OS Streptococcus uberis strain su-1 (ATCC 99277).
 PH key Location/Qualifiers
 FT Peptide
 FT 1..51
 FT /label= Sig-peptide
 FT /note= "alternative translation start site at Met-11"
 FT Protein
 FT 52..561
 FT /label= Mat-protein
 FT Region
 FT 148..199
 FT /note= "central repeated amino acid sequence A1"
 FT Region
 FT 200..212
 FT /note= "central repeated amino acid sequence B1"
 FT Region
 FT 213..271
 FT /note= "central repeated amino acid sequence C1"
 FT Region
 FT 282..325
 FT /note= "central repeated amino acid sequence A2"
 FT Region
 FT 326..339
 FT /note= "central repeated amino acid sequence B2"
 FT Region
 FT 340..397
 FT /note= "central repeated amino acid sequence C2"
 FT Peptide
 FT 525..530
 FT /note= "surface anchor motif"
 PN W09821231-A2.
 PD 22-MAR-1998.
 PF 14-NOV-1997; CA0867.
 PR 14-NOV-1996; US-031117.
 PA (UYGA-) UNIV SASRATCHEMAN.
 PI Jiang M, MacLachlan PR, Potter AA;
 DR WPI: 98-297860/26.
 DR N-PSDB; V42601.
 PT Immunogenic Streptococcus uberis protein(s) that bind bovine
 PT lactoferrin associated regulatory protein, useful in vaccines for
 PT treatment and prevention of mastitis
 PS Claim 2; Fig 2A-C; 105pp; English.
 CC This is the bovine lactoferrin binding
 CC Streptococcus uberis su-1. Its amino acid sequence was deduced
 CC from the novel isolated lbp gene (see V42601). The lbp is
 CC Lactoferrin species-specific; human lactoferrin does not
 CC effectively block binding of bovine lactoferrin. The invention
 CC provides recombinant vectors, transformed host cells and methods of
 CC producing recombinant bovine lbp of S. uberis. The bovine lbp,
 CC immunogenic fragments and/or chimeric proteins can be used, either
 CC alone or in combination with other antigens, in novel subunit
 CC vaccines for the prevention and treatment of S. uberis infections,
 CC particularly mastitis, as well as in diagnostic methods for
 CC determining the presence of S. uberis infections.
 SQ Sequence 561 AA.

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PT events, identify potential therapeutic agents, assess effects of
PT diet etc.
PS Disclosure; Pages 53-58; 75pp; English.

The sequence is that of a mutant rat alpha-myosin heavy chain which was used in the development of transgenic mammals, specifically mice. They can be used as a model for studying congestive heart failure (CHF) or hypertrophic cardiomyopathy. Such animals are used to study molecular and cellular events associated with CHF, to identify compounds for treating CHF, and in evaluating effects of diet and exercise on CHF. Conditions associated with CHF that can be evaluated this way are dilated or hypertrophic cardiomyopathy; acute aortic regurgitation; tricuspid stenosis; constrictive pericarditis; acute infective endocarditis; ischaemic heart disease; hypertension; primary myocardial disease; valvular or pericardial disease; hyperthyroidism; anaemia; arteriovenous fistula; beta-cell and Paget's disease.

Query Match 5.1%; Score 205.5; DB 1: Length 1886;
 Best Local Similarity 21.9%; Pred. No. 0.00014;
 Matches 116; Conservative 84; Mismatches 177; Indels 153; Gaps 22.

C 21 IVSRQQWVLLSDENRRLROELSECYEVARLOKVEI-ORVSEAVENLYKSSSKREA 79
 Db IIAKTKERRKLOEHAQDLDLOAEEDKVVTLTKSKVKLEQVYDDEGSLSEQEKVRMD 996
 QY 80 LEKAMRNLEGEIRMDHFNDRLEERLETANKOAEKYEYEGS-----EDPKTISOLFA 133
 Db 997 LERAKR-KLEGDIKLTGSSINDLEMDKRLQEKLEKKKFFDLSQONSKTEDECALALQLOK 1055
 QY 134 KNSQSRKEKYLEAL---ATKSTNE---DQRHHIFRDOALSNA-QAKVVKLEELK 185
 Db 1056 KLEKQAAIEELSELEERAKAVERKLRSDLRRELEIRLEERLEEAGAGSTVQJEMMKK 1115
 QY 186 KKQVYVKEVMQALYOLQA-----ACERKEOLEH--RLRPLEREIESURI 231
 Db 1116 REAEQKKRRDLEETLQHEATATARKKHNDVAELGEQIDNLRQVOKLEKEKSEKRL 1175

Dh	1176	ELDIWYSHNEQIIKAKANKEKESRTLEDOANEVRYKLEEAORSUNDFTTORAKIQOTENGE	1235
Qy	251	IMELLERKEERILALADMTKWEQ-----KYLE-----VYMRHFDALDA-----	291
Dh	1236	LAQOBEKEKELIMOLTRGLSTYQOMEDKRLQEBEGAKNALAH-ALQSRHDCDLRE	1294
Qy	291	-----ATVAARDTIVISHSPN-----TSYD-----ALEARIQKEE	323
Dh	1295	QVEEEMEAQAEIQR--VLSKANSFVAQWRKYETDIAIQRTLEBEAKKKIQAQGLQAAE	1351
Qy	324	FILMAKRCIDME-----GRITKLHQIILEKDMIKVLOQSRK-----EP	364
Dh	1352	AVAVANAKSLEKTKHRLQNEIEBIMADYVERSNAAAAALDKORNFDRKILAEKQKYE	1411
Qy	365	SKTEOLSCRRPAKS-----LMSISNAGSGLSHSPTLITGSPIMEKRDOKS	410
Dh	1412	SOSEELSSOKEARSLTELPRKIMAYFESIFHPTE-----KPKKN	1453

RESULT	15
W21731	
ID	W21731 standard; Protein; 2272 AA.
AC	W21731;
DT	31-OCT-1997 (first entry)
DE	GAL4/HA/NuMA fusion: protein.
KW	NIP-1; NIP-2; NuMA; nuclear mitotic apparatus; NuMA interacting protein
KW	cell division; proliferation; antibody; Ab; detection;
KW	malignant cell growth.
OS	Homo sapiens.
FT	key
FT	location/qualifiers
FT	1..147
FT	/label= GAL4 DNA binding domain

FT peptide 148..174
 FT /label= Hemagglutinin_epitope
 FT protein 175..2272
 FT /label= Residues_18-2116_of_NuMA
 FT 365..1864
 FT region /label= Coiled_coil_region
 PN MO9640917-A1.
 PD 19-DEC-1996.
 PF 07-JUN-1996; U09504.
 PR 07-JUN-1995; US-478408.
 PA (UYIA) UNIV YALE.
 PI McPherson SMG, Snyder MP;
 DR WPI: 97-077270/07.
 DR N-PSDB: 777782.
 PT New nucleic acid encoding nuclear mitotic appts. interacting
 PT proteins - useful for modulating cell division and proliferation and
 PT in diagnosis
 PS Claim 14; Page 28-36; 78pp; English.
 CC The sequences given in W21731-32 represent fusion proteins which contain
 CC NuMA (nuclear mitotic apparatus). The fusion proteins were used in
 CC the identification of NuMA interacting proteins (NIP's) (see also
 CC W21729-30). Compounds which interfere with the interaction of NuMA
 CC with a known NIP are used to modulate cell division and/or proliferation.
 CC Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to
 CC detect NIP (or their complexes) and to block their activity for
 CC diagnostic or therapeutic use, e.g. to detect defective NuMA or NIP
 CC which may be markers for aberrant (including malignant) cell growth
 CC (which can also be detected by nucleic acid sequencing). Also where
 CC malignancy is related to defects in NuMA or NIP, it can be treated by
 CC administration of the appropriate functional protein.
 SQ Sequence 2272 AA;

Query Match 6.1%; Score 204; DB 1; Length 2272;

Best Local Similarity 21.2%; Pred. No. 0.00022;

Matches 101; Conservative 82; Mismatches 163; Indels 130; Gaps 17;

OY 24 RAOQWVELSDENRNLROELBCEYKVARLQKVEITQVRSAYENVLYKSSKRALEKA 83
 DB 1156 RGQDEREVARLTQERGRADALALEKAR--AELEMLRNALNQRVEFATLOALAH 1212
 OY 84 MNKLEG---EIRRMHDFN-----RDLRELETANKOLAEKEYE---GS----- 122
 DB 1213 LTEX-EGKDOELAKRGLEAÑIKLEELROYKOLKEOLAKKEKHAHSGAOSEANGR 1271
 OY 122 -----EDTRKITSQLPANKKESQREKEKLEAELATARSTN-----BDQ 159
 DB 1272 TEPTGPKLEALRAEYVSKLEQCOQEOADSLERSLEAFERASRAERDSALETLQGLEK 1331
 O. 160 RHHIEIRDOALSNAQ-----AKVILEELKQKQYVYKVER-- 197
 DB 1332 AOELGHSQSALMSAORELAFFRTKYODHKAEDENKKAQVARGROAEKRNLSLSLEEV 1391
 OY 197 --MOQALVQ-----LOAACEKREOLEHRLR-----TRLEREL 226
 DB 1392 SILNROVLEKEGSEKELRLVMAESESOKLEERLRLLOAETASNSARAERSALREEV 1451
 OY 227 ESLRIQOQNGCQPTNWESEYVNAALMELLREKEERIALLEDMTKWEQKYLE-ENVMRHF 285
 DB 1452 QSLREAEKORVASEN-----LRQELTQAEFAEELGQELKAMQEKFFOKBOALSTL 1503
 OY 286 ALDAAATVAQRDTVISH--SPNTSYTALAEARTQKEE-----EILMANRC 332
 DB 1504 QLEHTSTALVSELLPAKHLCQLOAEOAAAEKRHREELQSKOAAGGLRAEELLRAOEL 1563
 OY 333 LDMEGRIKTLHAQIIEKDAMIKVLOORSRKEPSKTEQLSCMRPAKSIMSISNAGSG 388
 DB 1564 ----GELIPLNOKVAEE--RTAQQLRAEKAKASAEQSLMKKHGLAEENRGLG 1612

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OM protein - protein search, using sw model

Run on: January 18, 2000, 06:38:23 : Search time 132.79 Seconds
(Without alignments)
65.312 Million cell updates/sec

Title: US-09-332-063-2
Perfect score: 3347
Sequence: 1 MPRAQSSASQYGPADPFA.....KTPRIQLGQEPDAEMVEYLI 675

Scoring table: BLOSUM62

Searched: 130275 seqs, 12848600 residues

Da se : Issued_Patents_AA.*

Word size : 0

Number of hits that pass the threshold : 130275

1: /cgn2-6/ptodata/1/laa/5A.COMB.pep.*
2: /cgn2-6/ptodata/1/laa/5B.COMB.pep.*
3: /cgn2-6/ptodata/1/laa/PCTUS9.COMB.pep.*
4: /cgn2-6/ptodata/1/laa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	226.5	6.8	2482	1	US-08-328-254-6	Sequence 6, Appl1
2	225	6.7	3248	1	US-08-353-700-1	Sequence 1, Appl1
3	225	6.7	3248	3	PCT-US95-16216-1	Sequence 1, Appl1
4	213	6.4	262	1	US-08-403-379A-1	Sequence 1, Appl1
5	213	6.4	263	2	US-08-557-309B-51	Sequence 51, Appl1
6	213	6.4	262	2	US-08-929-414-1	Sequence 1, Appl1
7	209	6.2	219	2	US-08-557-309B-54	Sequence 54, Appl1
8	208.5	6.2	1248	2	US-09-080-897-2	Sequence 2, Appl1
9	204	6.1	2101	1	US-08-195-487-4	Sequence 4, Appl1
10	204	6.1	2101	3	PCT-US93-06160-4	Sequence 4, Appl1
11	203	6.1	576	2	US-08-533-306A-2	Sequence 2, Appl1
12	203	6.1	885	2	US-08-533-306A-4	Sequence 4, Appl1
13	203	6.1	816	2	US-08-533-306A-6	Sequence 6, Appl1
14	203	6.1	576	2	US-08-742-923A-2	Sequence 2, Appl1
15	203	6.1	885	2	US-08-742-923A-4	Sequence 4, Appl1
16	203	6.1	816	2	US-08-742-923A-6	Sequence 6, Appl1
17	203	6.1	180	4	5273901-7	Patent No. 5273901
18	203	6.1	180	4	5483709-6	Patent No. 5483709
19	201.5	6.0	2101	1	US-08-466-390-4	Sequence 4, Appl1
20	201.5	6.0	2101	1	US-08-470-950-4	Sequence 4, Appl1
21	201.5	6.0	2101	1	US-08-467-781-4	Sequence 4, Appl1
22	201.5	6.0	2101	2	US-08-483-924-4	Sequence 4, Appl1
23	199.5	6.0	1388	2	US-08-685-576-4	Sequence 4, Appl1
24	199.5	6.0	1388	2	US-08-685-576-4	Sequence 4, Appl1
25	199	5.9	1255	2	US-09-080-897-4	Sequence 4, Appl1
26	197.5	5.9	1388	2	US-08-685-576-1	Sequence 1, Appl1
27	193.5	5.8	955	1	US-08-006-676B-1	Sequence 1, Appl1
28	193.5	5.8	955	1	US-08-282-845-2	Sequence 2, Appl1
29	193.5	5.8	955	3	PCT-US94-00324-1	Sequence 1, Appl1
30	191	5.7	1093	3	PCT-US93-03077-1	Sequence 1, Appl1
31	187.5	5.6	466	1	US-08-450-360-2	Sequence 1, Appl1
32	184.5	5.5	1898	1	US-08-056-200-94	Sequence 94, Appl1
33	184.5	5.5	1898	2	US-08-600-644-94	Sequence 94, Appl1
34	183	5.5	677	1	US-08-188-582-13	Sequence 13, Appl1
35	183	5.5	677	1	US-08-646-715-13	Sequence 13, Appl1

36	178.5	5.3	214	1	US-08-217-327-4	Sequence 4, Appl1
37	177.5	5.3	1298	2	US-08-690-473-2	Sequence 2, Appl1
38	176.5	5.3	98	2	US-07-814-220-2	Sequence 2, Appl1
39	176.5	5.3	98	2	US-07-812-421-2	Sequence 2, Appl1
40	176.5	5.3	683	4	5210183-3	Patent No. 5210183
41	176	5.3	900	2	US-08-630-822A-62	Sequence 62, Appl1
42	176	5.3	900	2	US-09-005-069-62	Sequence 62, Appl1
43	173	5.2	1719	2	US-08-459-568-4	Sequence 4, Appl1
44	173	5.2	1719	2	US-08-399-411-4	Sequence 4, Appl1
45	173	5.2	443	2	US-08-795-475-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-328-254-6
Sequence 6, Application US/08328254
Patent No. 5710022
GENERAL INFORMATION:
APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A NO. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2482 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-254-6

Query Match 6.8%; Score 226.5; DB 1; Length 2482;
Best Local Similarity 21.4%; Pred. No. 6.1e-07;
Matches 139; Conservative 100; Mismatches 233; Indels 179; Gaps 26;

26 GQWEILSDNRNRCGE-----GCYEVARLQKVEIRVSRAVENLWSSKRE 78
149 QDLEVLQSSYKLNLELETKDKMSFEYKVKRAKTELDOR--EMHMAQTELOE 2005
79 ALEKAMPKLEGEIRRMHD-----FNDLRELEFANKQLAEKEEGESD- 124
2006 EL-SGENRLAGELQILLEIKSSQDLKELLLENELKKSIDCMKRDQYKRGYREI 2064
124 -----TKRTISQLEPAKKNESQREKKLEAEIATARSTNEDQRRHIEI---RDQAL 170

Db 2065 AEYOLRLHEAEKHHQALLDITNKQVEIOTYREKLSKEECLSSQKLEIDLKSSKEEL 2124

QY 171 SNAARVYKLEELKKVY-----YDKV-----EKKQALVOLQAAECERQLEHRLTRL 222

Db 2125 NNSLKATQIIEELKTRKMDLKYVNOQLKENERAOGKMKILIKSCQLEKEKLEIQLKEL 2184

QY 223 ERELESIRIOOGNCOPTVSEYNA--AALMELLREKEEELIALLADMTMEQKYLEEN 280

Db 2185 S-QLQAAOERKOTGTVDKDELTEIKELKLEELK-----TKADEYLDKY 2232

QY 281 VMRHFLDAATVAOBDTIVYSHSPNTSYDTALEARIOKEEELIANKKCLMEGRK 340

Db 2233 C-----SLISHE-----KLEKAKEM-----LETOVA 2254

QY 341 TLHAQIIEKDA-----MIKVLQOORSRKEPSKTEOLSCMPAKLSISNAGSLSHSSTL 396

Db 2255 HLCSQOKSDRSGPLGPPVPGSPPIPSYTE-----KRLSSGQKMSQKGRORSSGI 2306

QY 397 TGSIMEKRDKWKSGSLGILLGODVRAEIVPSTPSPVPTLLSAHSKTSGRDCSTQ 456

Db 307 -----WENG-----PTPAPPESEFSKSKKRAVMGSIHPAE 2337

QY 457 TERGESNKTAAVAPISVPAPVAAATAATATATAT--TTTVAAPAVAVAAAAA 514

Db 2338 DTBCTE-----FEPEGLPEVYKKGFPADIPGKTSPIILRRITW----- 2376

QY 515 AAAPSPATAATAAASPAAGQIPAAASVAAAAPSAAAAAAAYVAPAPAPVAPA 574

Db 2376 ATRTSP-RLAAQKIALSLPSLGKRENLAS-----SKPTGSGSQQKVKYQARSPVSGT 2428

QY 575 LVPPAPAAAQASAPACTOAPTSAPAAVPTPAPPTPAPVAAOAVPASPATG 625

Db 2429 ILREP-----TTKSVV-----NNLPERSPTDSPREGLRVKGRLVPSPKAG 2470

RESULT 2

US-08-353-700-1

Sequence 1, Application US/08353700

Patent No. 5599919

GENERAL INFORMATION:

APPLICANT: YEN, TIMOTHY J.

APPLICANT: RATTNER, JEROME B.

TITLE OF INVENTION: NUCLEIC ACID ENCODING A

TITLE OF INVENTION: TRANSLIENTLY-EXPRESSED KINETOCHORE PROTEIN.

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN

STREET: 1601 MARKET STREET, SUITE 720

CITY: PHILADELPHIA

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/353,700

FILING DATE: 09-DEC-1994

CLASSIFICATION: 433

ATTORNEY/AGENT INFORMATION:

NAME: REED, JANET E.

REGISTRATION NUMBER: 36,252

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 563-4100

TELEFAX: (215) 563-4044

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3248 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: HUMAN

US-08-353-700-1

Query Match 6.7%; Score 225; DB 1; Length 3248;

Best Local Similarity 21.4%; Pct. No. 1.1e-06;

Matches 110; Conservative 106; Mismatches 167; Indels 132; Gaps 21;

QY 20 AIVSRAQOMVEILSDENRNLROELGCEYKVARLQK-----VETEIQRVSAYE 68

Db 2103 AEVKEKELLQTLSSDVSELLKDKTHLOEKLOSLEKDSQALSLTKCELENOIQLNKEKE 2162

QY 69 NLYKSSSK-----REALKAMRKLEGEIR-----RMHDFNR-----DLRE 104

Db 2163 LLYVESESLQARLSESDYEKLNVSKALAEALVKEGFEALALSSTOEYVHQLRGIEKLRV 2222

QY 105 RLEFANKQ--LAEK-----EYEGSEDTRKTTISQLFANKRESOR--EKEKLEAELAT 151

Db 2223 RIADKKOLHIAEKLERERENDSLDKVYENLERELQNEQELVYILDENSKAEVET 2282

QY 152 ARSTNEQORRHIEIRDOALSNQAKYKLEELKKQOVYVDYKEM-----QQA 200

Db 2283 LKTOIEEMASLKFELDTLTLSKEXENLTKOIEROGOLSELDKLSFSKSLLEKEQA 2342

QY 201 LVOLQ-----AACERK-----OLEHRLTRLERE 225

Db 2343 EIDIKESKTAIVEMLQNLKELNEVAALCGDQEIKNKATQOSIDPPIEEHQLNRSLEKL 2402

QY 226 LESLRIOQROGNC--OPTNVSEYNAAL-----MELLEKEERILALADMTKWE 273

Db 2403 RARLEADEKKQCLVLOOLKESEHADLLKGRVENLERELEIARTNOEH--ALAEANSKGE 2461

QY 274 OKYLEERV-----MRHFLDAAA-----VVAQOROTTVISHP--NTSIDTALEAR 317

Db 2462 VETLKAKIEGMSLOSLGLELDVVTINSEKENLTNELQKEQERISELEIINSSENTLO-- 2520

QY 318 IOREEBELMANRCIDMEGRINTLHAQIIEKDMATIKVLOQORSR--KEPSKTEQLSC--MR 374

Db 2520 -EREQEKYQKKESSAME--MLOTQKELNERVAALHNOEACAKAEONISSVECLELE 2577

QY 375 PAKSLMSISNAGSLSHSSTTGTSPIMEKRDCK 409

Db 2578 KAOLLOGLDEAKNNYIVLQSVKG--LIOEVEDGK 2610

RESULT 3

PC9-US95-16216-1

Sequence 1, Application PC/TUS9516216

GENERAL INFORMATION:

APPLICANT: Yen, Timothy J.

APPLICANT: Rattner, Jerome B.

TITLE OF INVENTION: Nucleic Acid Encoding a Transiently

TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann, Dorfman, Herrell and Skillman

STREET: 1601 Market Street Suite 720

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/16216

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Page 3

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
X-POTENTIAL: NO
ANTI-SENSE: NO
PCT-US95-16216-1

Query Match 6.7% Score 225; DB 3; Length 3248;
Best Local Similarity 21.4%; Pred. No. 1.1e-06;
Matches 110; Conservative 106; Mismatches 167; Indels 132; Gaps 21;

QY 20 AIVSRAQOMWELSDENRNLROELGCEKVAARQK-----VETEIQRVSEAYE 68
DB 2103 AEVKEKTELLDTSSDVSELKDKTHLOEKLSLEKDSOALSLTKCELHNOIAQLNKEKE 2162
QY 69 NIVKSSSK-----REPLEKAMRNLEGEIR-----RMHDPNR---DLRE 104
DB 2163 LIVVSESSLOARLSESDYKINWASKALBAALVEGEPALRLSTQOEVOHQRLRIETKRLV 2222
QY 105 RLEATANKO---LAER-----EYEGSEDTRKTIQSOLFAPKNESOR---EKEKLEAEIAT 151
DB 2223 RIEADEKQOLHIAEKLKERERENDSLDKVNLERELQMSSENLVILDAENSKAEVET 2282
QY 152 ARSINEQQRHIEFDALSAQAQKVVLEELKKQVYVVKVEM-----QQA 200
DB 2283 LKQIEEMARSLKIFELDLVTLRSEKENLTKQIOEKQGLSELDKLSFSLKEKQA 2342
QY 201 LVOLQ-----AACERK-----QLERLTRLEIRE 225
DB 2343 EIOIKESKRAVEMLOQLKELNEVAALCGDOEIMKATQSLDPIEEHQLNRSIEKL 2402
QY 226 LESLRIOQROGNC---QPTNVSEVNAAL-----MELLREKEERITALEADMTKWE 273
DB 2403 RARLEADEKQOLCVLQOLKESSEHADLLKGVNLEKERELEIARTNOEH--AALEKNSKE 2461
QY 274 QKYLEENV-----MRHAFALDAAA-----TVAAQRDTTVISHSP--NTSYDTALEAR 317
DB 2462 VETLKAKIEGTMOSLRGLLELDVVTIRSEKENLTKQIEKQERISELIISSSEFNILQ-- 2520
QY 318 IOKEEELILANRCLDMERITLHNOIEKDMITVLOORS--KEPSTEOIISC--MR 374
DB 2520 -EKEOEVOOKESSTAME-MIOTQKELNEVAALHNDDEACKAKBONLSQVECELE 2577
QY 375 PAKSLMSISNAGSLSHSSTLTGSPIMEERDOK 409
DB 2578 KAOLOGLDCAKNNYIVLQSSVAG--LIOEVEBOK 2610

RESULT 4
US-08-403-379A-1
Sequence 1, Application US/08403379A
Patent No. 5756662
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION
OF T. CRUZI INFECTION
NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 F.Fth Avenue
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,379A
FILING DATE: 14-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-403-379A-1

Query Match 6.4% Score 213; DB 1; Length 262;
Best Local Similarity 48.4%; Pred. No. 2.8e-07;
Matches 74; Conservative 9; Mismatches 54; Indels 16; Gaps 9;

QY 479 AATATAATATATATTTTVAAP---VAVAAAPADA-AAAPSPPTAATAAASPA 534
DB 112 AA-AAAARKORAAKK-----AAAPSGKSKAKAIAAPAKAAAPAKAAAPAK 165
QY 535 AGOIPAAASVASA-AAVAPSAASAAAQVAPAPAPAPALVVPAPAAQASAPQTO 593
DB 166 AAAAPAPAAAPAAAPAAAPAKAAAPAKTA-AAAPAKAAAPAKA-AAAPAKA-ATAAPAKAA 222
QY 594 AFTSAPVAPPTPTPTPTPAVVOAEVPPASPATGP 626
DB 223 AAPAKATAPAKAAT-APAKA-AAAPAKATAP 253

RESULT 5
US-08-557-309B-51
Sequence 51, Application US/08557309B
Patent No. 5916572
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND
PREVENTION OF
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids

US-08-557-309B-54

D5 476 APVAAAAATAATTAATTITTTMVAAAPVAVAAAAAABAAAASPDATA-----A 528
| | ||| : | ||| |||| | ||| |
58 AAAAAKQAAAAKKAAPSGCKSAKAAAP--AKAAAAAPKAAAPPRAKTAAAPAKAAAHAKA 115

QY 529 AVSPAAGQIPAAASVSAANAANVAPSAANAQVAPAPAPAPALVPPAPAPAAQASA 588
 DB 116 AAPPAKAAAPPAKTAAPPAKTAAPPAKAAAPPAKAAAPPAKAAAPPAKAAAPPAKAA 174
 QY 589 PAQOAPTSAPAVAP 626
 DB 175 PAKAAAPPAKAAAPPAKAAAP-PAKAAAP-PAKAAAPAP 210

RESULT 8
 US-09-080-897-2
 Sequence 2, Application US/09080897
 Patent No. 5985574

GENERAL INFORMATION:

APPLICANT: King, Mary-Claire
 APPLICANT: Lynch, Eric D.
 APPLICANT: Lee, Ming
 APPLICANT: Morrow, Jan E.
 APPLICANT: Welch, Piri L.
 APPLICANT: Leon, Pedro E.
 TITLE OF INVENTION: Modulators of Actin
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAM GROUP
 STREET: 75 DENISE DRIVE
 CITY: HILLSBOROUGH
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94010

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/080.897
 FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: UW97-001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 343-4341
 TELEFAX: (650) 343-4342

FORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1248 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-080-897-2

Query Match 6.2%; Score 208.5; DB 2; Length 1248;
 Best Local Similarity 20.4%; Pred. No. 4e-06;
 Matches 162; Conservative 95; Mismatches 274; Indels 263; Gaps 39;

QY 7 SSASQVPP-ADPAFAVRAQOMV-----ELSDENR-----LNQLEGCEK 49
 DB 62 SSASGDPPTQOSLODVSDVVLPEQMLDMNNEKQOPLRKKDITIRKENVSYLY 121
 QY 50 VARLOKVELEQVSEAYENLVKSS-----SKREALEKARN-----K 87
 DB 122 TSQKMSQKSSKSMYIOELRSLRDMPLSLCSLSLVSINNPNVSVWOTFGAGLAS 181
 QY 88 LEGERRHNDPRLRELETRANKOLAKEVEGSEDTK-----TISQFAKKNKESQREK 142
 DB 182 LLDLTKRLHD-----FKRETA-----GSYDSRNKHEIILCLAFNMNKFQ----- 222
 QY 143 EKLEALFATSTNEDQRRHIEIRQALSNQAKYVKL-----EELKKK----- 188

DB 222 -----IKTMEETFGILLVRAAMPVPMITDAKLISALCITLPOEDMNERVLEANT 275

QY 188 -OVYDKVEKMOAL-----VOLQAC-----EKROLEHRLTLE----- 224

DB 276 EREMDFEYERFQPLDLGKSGTTIALKVGCLOLINALTPARELDFRHIRSELNRLGILH 335

QY 224 -----RELK-----LTIQ-----ORQNCOP-----TIVSEYNA-----ALMELLREK 258

DB 336 QVLDIPELENDMDRVQNVNDEDEEDSYDLKGRILDIRMEDDFNEVFQILLTVKDS 395

QY 259 E-----ERILAEADMTKEOKY-----LEENV-----MRHFDLDAAT 292

DB 396 KAEHFLSLQHLVRYNDYKAPQYVILIECISQIYLHKRGADPDFKCRLOTEIEGL 455

QY 293 VAAQDQTVISHSP-----NTSYDTALEARIQKEEELIMANKRCLDMEGRITLHAQI 346

DB 456 IDQMDIKTKVESEAKALEKLDSELTARHELOVEKKNES-----DFEQKLOLOG-- 510

QY 347 IENQAMIVLOQSRKSPKSPKTPOLSCMRPAKSLMSISNAGSGLSHSSTLIG--SPIMEE 404

DB 510 -EKDAL-----HSEKQOIAEK-----QLEAEVSQLTGEVAKLKE 545

QY 463 KPDKSWKSGILGQYRAEYVSTPS--PVPSSTPLSHSKTGSRCSTQTERGTE 462

DB 546 LEDAKKEMASLSA-----ATVPSVPSRAVPVPPAPL-----PQDSGT- 586

QY 463 SNKTAAVAPISVPAVAAATAATATATATTTVAAPVAAVAAAP-----AAAASP 520

DB 586 -----IIPPPAPGD-----STIPPPPPPPPPPPPPPGTALISPPP 623

QY 521 ATAAATAAVSPAAG-QIPAAASVSAANAANVAPSAANAQVAPAPAPAPAPAPAPAPAP 578

DB 624 LSGDATIPPPPLPEGVGIPSSILPGCTAIPPPPLPGSARI--PPPPPLPGSAGIIPP 682

QY 579 PAPAQAQSAQAQAPASAPAVATP-----APTTPVAQAE-----VASPAT 624

DB 683 PPPLPGEGMPPPPPLPGGCGIIPPPPGGCGIIPPPPGMGMPPPPGGVPAAVVL 742

QY 625 --GPGHRSIPSL 636

DB 743 PEGILPKKLYREV 756

RESULT 9
 US-08-195-487-4
 Sequence 4, Application US/08195487
 Patent No. 5783403

GENERAL INFORMATION:

APPLICANT: YODKATLY, GARY
 APPLICANT: LIDGARD, GRAHAM F
 TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
 TITLE OF INVENTION: INTERIC NUCLEAR MATRIX
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: TESTA HUMMIX & THIBEAULT
 STREET: 53 STATE STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/195.487

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/901.701

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-195-487-4

Query Match 6.1%; Score 204; DB 1; Length 2101;
Best Local Similarity 22.3%; Pred. No. 1.5e-05;
Matches 106; Conservative 78; Mismatches 163; Indels 128; Gaps 19;

24 RAQOMVELSDENRNLROELGCTEVARLOKVETEIORVSEAYENLVKSSKREALEKA 83
DB 999 RGOOEREVARLTORERGAQADLALEKAR---AELEMRLOALNEORVEFATLQALAH 1055
84 MRNKLGE---EIRRMHDE---RDLERELETANKOLAEKYE---GS----- 122
DB 1056 LTER-EGKDELAKRLGLEAQAQKELEELRQTVKQLEQAKKEKHAASGSGAOSAGR 1114
122 -----EDTKRTISQLEFANKESOREKEKLEAEIATARSTNEDORRHIEIDQALSNA 173
DB 1115 TEPTGPKLEALRAVEKSKLEQCCQKQOQADLSLEKASRAE-----RDSLETL 1167
174 QAKVVKLEELKKQ-----VYDKYKMOQALVOLQAAECR-REOLEHR--LR 219
DB 1168 OGQLEEKAGELGHSQSALASAGRELAFAFTKYVDHSHKADEMKAAQVARGQEAERKNSLI 1227
220 TRLEREL-----ESLRIOQRGNC-----QPTNVEYNAAA 250
DB 1228 SLEEEVSHINROYLEKESKELRLVMAESKSOKEESCACCRORPATVPELONAA 1287
251 LM-----ELLRE---KEERILALEADMTKWEOKYLE-ENVVRHFA 286
DB 1288 LIGRCRCASGRAEAKORVASENLRQELTSGARAEELGQELKAKQEFKQKQALSTIQ 1347
287 LDAATVAAGQDVTYISH--SPNTSYDTALFARIQKEE-----EILANKRCL 333
DB 1348 LEHTSTQALVSEILPAKHLCQQLAQAARAEKRRHELEQSKQAAGGLRAELRAQREL- 1407
334 DMEGRITLHAQIIEKDMIKVLOQRSKREKPESTEDLSGMRPAKSLMSISNAGSG 388
DB 1407 ---GELIPLKQKVAEDD---RTAQQLRAEKASYAEQSLMKRAHGLLAENRGLG 1455

RESULT 10
PCT-US93-06160-4
Sequence 4, Application PC/TUS9306160
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/06160
FILING DATE: 19930621
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-06160-4

Query Match 6.1%; Score 204; DB 3; Length 2101;
Best Local Similarity 22.3%; Pred. No. 1.5e-05;
Matches 106; Conservative 78; Mismatches 163; Indels 128; Gaps 19;

24 RAQOMVELSDENRNLROELGCTEVARLOKVETEIORVSEAYENLVKSSKREALEKA 83
DB 999 RGOOEREVARLTORERGAQADLALEKAR---AELEMRLOALNEORVEFATLQALAH 1055
84 MRNKLGE---EIRRMHDE---RDLERELETANKOLAEKYE---GS----- 122
DB 1056 LTER-EGKDELAKRLGLEAQAQKELEELRQTVKQLEQAKKEKHAASGSGAOSAGR 1114
122 -----EDTKRTISQLEFANKESOREKEKLEAEIATARSTNEDORRHIEIDQALSNA 173
DB 1115 TEPTGPKLEALRAVEKSKLEQCCQKQOQADLSLEKASRAE-----RDSLETL 1167
174 QAKVVKLEELKKQ-----VYDKYKMOQALVOLQAAECR-REOLEHR--LR 219
DB 1168 OGQLEEKAGELGHSQSALASAGRELAFAFTKYVDHSHKADEMKAAQVARGQEAERKNSLI 1227
220 TRLEREL-----ESLRIOQRGNC-----QPTNVEYNAAA 250
DB 1228 SLEEEVSHINROYLEKESKELRLVMAESKSOKEESCACCRORPATVPELONAA 1287
251 LM-----ELLRE---KEERILALEADMTKWEOKYLE-ENVVRHFA 286
DB 1288 LIGRCRCASGRAEAKORVASENLRQELTSGARAEELGQELKAKQEFKQKQALSTIQ 1347
287 LDAATVAAGQDVTYISH--SPNTSYDTALFARIQKEE-----EILANKRCL 333
DB 1348 LEHTSTQALVSEILPAKHLCQQLAQAARAEKRRHELEQSKQAAGGLRAELRAQREL- 1407
334 DMEGRITLHAQIIEKDMIKVLOQRSKREKPESTEDLSGMRPAKSLMSISNAGSG 388
DB 1407 ---GELIPLKQKVAEDD---RTAQQLRAEKASYAEQSLMKRAHGLLAENRGLG 1455

RESULT 11
US-09-533-306A-2
Sequence 2, Application US/08533306A
Patent No. 5837457
GENERAL INFORMATION:
APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for Detection of Chromosome 16
TITLE OF INVENTION: Rearrangements
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harless, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI

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us-09-332-063-2.ra1

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COUNTRY: USA
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 2115-00869COB
FILING DATE: September 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Dean F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-00869COB
TELEPHONE: (810) 641-1600
TELEFAX: (810) 641-0270
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-533-306A-2

Query Match 6.1%; Score 203; DB 2; Length 576;
Best Local Similarity 23.4%; Pred. No. 3.5e-06;
Matches 101; Conservative 74; Mismatches 150; Indels 106; Gaps 16;
QY 30 EILSDENRNL---OELEGCEYKVARLOKYTE-----IORVSEAVENLYKSSSKREA 79
DB 192 ELQASEDKKLRLVNMQALKGQFERDLQARDQNEKRRQLOROLHEYTELEDERNERA 251
QY 80 LEKARNKLEGEIRRMHDFNRLRELETANKQLAE-----KEYGGS-EDTRKTSQLFA 133
DB 232 LAAAKKLEGLDLQADSAIKGREALIKQLKLOAKMDQRELEDAKASDELIFA 311
QY 134 NKESQR-----EKEKLEALATA---RSTNEDQRRH 162
DB 312 TAKENKAKSLLEADLMQLOEDLAAERARQADLEKELELASSLSGRNALODEKRR 371
QY 163 IEIRQALSNQAKVVKLEELKKQ---VYDVKEMQALVOL--QACER-REOLE 215
DB 372 LE-----ARLAOLEELEEDQNGMEASDRVRATQOABOLSNELATERSTAKN 421
QY 216 HRLRRLERELESRLIOQROGNCOPTNVSEYNAALMELREKEERILALADMTKWKQ 275
DB 422 ESARQOLERQKELR-----SKLHEMGAVKSKF---KSTIALLEAKTIAQ----- 464
QY 276 YLEENVMHFLDAAATVAOQDITVISHSPNTSYDTALEARIQKEEELIMANKRCIDM 335
DB 464 LEEGVQEARQKQATSKLQK-----DKKLKELLQVDEKRAKAEQYKQEA 510
QY 336 E---GRITLHAQIIEKAMIKVLOQSRKPESTEQLSCHMRPAKSLMSISNAGSLISH 392
DB 511 EKGARVQOLKRLQLEAEESQRIANRRKILQREIDEATESNEA-----MGREVAL 562
QY 393 SSTLTGSPIME 403
DB 563 KSKLGRPPQE 573

RESULT 12
US-08-533-306A-4
Sequence 4, Application US/08533306A
Patent No. 5837457
GENERAL INFORMATION:
APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David

TITLE OF INVENTION: Markers for Detection of Chromosome 16
NUMBER OF INVENTION: Rearrangements
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: USA
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 2115-00869COB
FILING DATE: September 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Dean F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-00869COB
TELEPHONE: (810) 641-1600
TELEFAX: (810) 641-0270
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 885 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-533-306A-4

Query Match 6.1%; Score 203; DB 2; Length 885;
Best Local Similarity 23.4%; Pred. No. 6e-06;
Matches 101; Conservative 74; Mismatches 150; Indels 106; Gaps 16;

QY 30 EILSDENRNL---OELEGCEYKVARLOKYTE-----IORVSEAVENLYKSSSKREA 79
DB 501 ELQASEDKKLRLVNMQALKGQFERDLQARDQNEKRRQLOROLHEYTELEDERNERA 560
QY 80 LEKARNKLEGEIRRMHDFNRLRELETANKQLAE-----KEYGGS-EDTRKTSQLFA 133
DB 561 LAAAKKLEGLDLQADSAIKGREALIKQLKLOAKMDQRELEDAKASDELIFA 620
QY 134 NKESQR-----EKEKLEALATA---RSTNEDQRRH 162
DB 621 TAKENKAKSLLEADLMQLOEDLAAERARQADLEKELELASSLSGRNALODEKRR 680
QY 163 IEIRQALSNQAKVVKLEELKKQ---VYDVKEMQALVOL--QACER-REOLE 215
DB 681 LE-----ARLAOLEELEEDQNGMEASDRVRATQOABOLSNELATERSTAKN 730
QY 216 HRLRRLERELESRLIOQROGNCOPTNVSEYNAALMELREKEERILALADMTKWKQ 275
DB 731 ESARQOLERQKELR-----SKLHEMGAVKSKF---KSTIALLEAKTIAQ----- 773
QY 276 YLEENVMHFLDAAATVAOQDITVISHSPNTSYDTALEARIQKEEELIMANKRCIDM 335
DB 773 LEEGVQEARQKQATSKLQK-----DKKLKELLQVDEKRAKAEQYKQEA 819
QY 336 E---GRITLHAQIIEKAMIKVLOQSRKPESTEQLSCHMRPAKSLMSISNAGSLISH 392
DB 820 EKGARVQOLKRLQLEAEESQRIANRRKILQREIDEATESNEA-----MGREVAL 871
QY 393 SSTLTGSPIME 403
DB 872 KSKLGRPPQE 882

RESULT 13

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Db 422 ESAROLERONEKLR-----SKLHEMGAVSKF-----KSTIALEAKIAQ-----464
Qy 276 YLEENVMRHFALDAATVAARDTVISHSPNTSYDTALEARIOKEEELIANKRCIDM 335
Db 464 -LEEQVEQEARREKQATSKLQK-----DKRLKEILLQVEDERKMAEQYKEQA 510
Qy 336 E---GRITLHAQIIEKDMITVLOORSRKEPSKTEQLSCMRPAKSLMSISNAGSGLSH 392
Db 511 EKGNAHVQLKROLEAEESQRIANRRKIQREIDEATESNEA-----MGREYNAL 562
Qy 393 SSTLGSPIME 403
Db 563 KSKLNGPPPOE 573

RESULT 15
US-08-742-923A-4
Sequence 4, Application JS/08742923A
ent No. 5869611

GENERAL INFORMATION:
APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for Detection of Chromosome 16
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: USA
ZIP: 48303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742.923A
FILING DATE: No. 5869611 member 1, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Dean F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-00869DVC
TELEPHONE: (810) 641-1600
TELEFAX: (810) 641-0270
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 885 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-742-923A-4

Query Match 6.1%; Score 203; DB 2; Length 885;
Best Local Similarity 23.4%; Pred. No. 6e-06;
Matches 101; Conservative 74; Mismatches 150; Indels 106; Gaps 16;

Qy 30 EISDENRNR-----QELCECYKVARLOKETE-----IQRVSEAYENLVKSSSKREA 79
Db 501 ELQSEDAKRLLEVMNMAKQFQERDQARDEQNEERROLOQROLHEVETELDERNERA 560
Qy 80 LEKAMRNKLEGEIRRMHNDLRELETANKOLAE-----KEYEGS-EDRKITSQDLFA 133
Db 561 LAAAKKKLEGDLDLQADLSAIGREAIKQRLQAOQKDFORELEDAARASRDEIFA 620
Qy 134 KNEQSQR-----EKEKLEAEIATA-----RSTNEDORRH 162

Db 621 TAKENFKKRLSLADLMQLOEDLAAAFARARQADLEKEELAEELASSISGRNALODEKRR 680
Qy 163 ITRQALSNQAKVYKLEELKKQ-----YVDKVEKQOALVOL--QACER-REOLE 215
Db 531 LE-----ARIQOLEEELQEGNMMAESDVRKATQOAEQLSNELATERSTQAKN 730
Qy 216 HRLFTRELESLRIQROGNCOPTNVSEYNAALMELLEKEERITALEADMTKWEQ 275
Db 731 ESAROLERONEKLR-----SKLHEMGAVSKF-----KSTIALEAKIAQ-----773
Qy 276 YLEENVMRHFALDAATVAARDTVISHSPNTSYDTALEARIOKEEELIANKRCIDM 335
Db 773 -LEEQVEQEARREKQATSKLQK-----DKRLKEILLQVEDERKMAEQYKEQA 819
Qy 336 E---GRITLHAQIIEKDMITVLOORSRKEPSKTEQLSCMRPAKSLMSISNAGSGLSH 392
Db 820 EKGNAHVQLKROLEAEESQRIANRRKIQREIDEATESNEA-----MGREYNAL 871
Qy 393 SSTLGSPIME 403
Db 872 KSKLNGPPPOE 882

Search completed: January 18, 2000, 06:46:52
Job time: 509 sec

